SEQUENCE LISTING

<110> Allen, Keith D. <120> TRANSGENIC MICE CONTAINING INWARDLY RECTIFYING POTASSIUM CHANNEL (Kir5.1) GENE DISRUPTIONS <130> R-902 <150> US 60/254,888 <151> 2000-12-11 <160> 4 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1257 <212> DNA <213> Mus musculus <400> 1 atgagetatt aeggaagtag etaceggatt gteaatgtgg aetecaaata teeaggetat 60 cctccagagc atgccatcgc tgagaagaga agagcaagaa ggcgcttgct ccacaaagat 120 ggcagctgta atgtgtactt taaacacatt tttggagaat gggggagcta catggttgat 180 atttttacca ctcttgtgga taccaagtgg cgccatatgt tcataatatt ttctctgtct 240 tacattetet cetggttgat atttggttee atattttgge teatageett teateaegga 300 gacctattaa gcgatccaga tatcacccct tgtgttgaca acgtgcattc atttacggct 360 gcatttttat tetecetgga gaeceagaee accattggat aeggttaeeg etgtgteaee 420 gaagagtgct ctgtggctgt actgacagtg atccttcagt ccatcctcag ctgcatcata 480 aacaccttca tcattggagc agccttggca aagatggcaa ctgcccggaa gagagcccag 540 accatacgct tcagctattt tgccctcatt ggtatgagag acgggaagcc ttgcctcatg 600 tggcgcatag gtgacttccg accaaaccat gtggtagagg gcacggtgag agcccaactt 660 ctgcgctatt cagaagacag tgaagggagg atgacgatgg cgtttaaaga cctcaaactc 720 gtcaatgacc agataatcct ggtaactcca gtgactattg tccatgaaat tgaccatgag 780 agccctctgt atgcccttga ccgcaaggca gtggccaaag ataatttcga gattctggtg 840 acatttattt atactggtga ttccactggg acatcccacc agtccagaag ttcctacatc 900 cccagagaaa ttctctgggg ccacaggttt catgatgtat tggaagtgaa gagaaagtac 960 tacaaggtga actgcttgca gtttgaagga agcgtggaag tctacgcccc cttttgcagt 1020 gccaaacaac tggactggaa ggaccaacaa ctcaacaact tggagaaaac gtcccctgcc 1080 cgaggatcct gcaattctga caccaacacc aggaggcggt ccttcagcgc agttgccgtg 1140 gtgagcagct gtgagaaccc agaggagacc gtcctgtccc cacaagatga atgtaaggag 1200 atgccctatc agaaagccct cctgacttta aataggatct ccatggaatc ccagatg <210> 2 <211> 419 <212> PRT

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 25
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 Arg Arg Arg Leu Leu His Lys Asp Gly Ser Cys Asn Val Tyr Phe Lys
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 His Ile Phe Gly Glu Trp Gly Ser Tyr Met Val Asp Ile Phe Thr Thr
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Leu Val Asp Thr Lys Trp Arg His Met Phe Ile Ile Phe Ser Leu Ser

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Tyr Ile Leu Ser Trp Leu Ile Phe Gly Ser Ile Phe Trp Leu Ile Ala
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Asp Asn Val His Ser Phe Thr Ala Ala Phe Leu Phe Ser Leu Glu Thr
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Gln Thr Thr Ile Gly Tyr Gly Tyr Arg Cys Val Thr Glu Glu Cys Ser
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Val Ala Val Leu Thr Val Ile Leu Gln Ser Ile Leu Ser Cys Ile Ile
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Asn Thr Phe Ile Ile Gly Ala Ala Leu Ala Lys Met Ala Thr Ala Arg
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Lys Arg Ala Gln Thr Ile Arg Phe Ser Tyr Phe Ala Leu Ile Gly Met
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Arg Asp Gly Lys Pro Cys Leu Met Trp Arg Ile Gly Asp Phe Arg Pro
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Asn His Val Val Glu Gly Thr Val Arg Ala Gln Leu Leu Arg Tyr Ser
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                                             220
Glu Asp Ser Glu Gly Arg Met Thr Met Ala Phe Lys Asp Leu Lys Leu
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Val Asn Asp Gln Ile Ile Leu Val Thr Pro Val Thr Ile Val His Glu
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Ile Asp His Glu Ser Pro Leu Tyr Ala Leu Asp Arg Lys Ala Val Ala
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Lys Asp Asn Phe Glu Ile Leu Val Thr Phe Ile Tyr Thr Gly Asp Ser
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                                                 285
Thr Gly Thr Ser His Gln Ser Arg Ser Ser Tyr Ile Pro Arg Glu Ile
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Leu Trp Gly His Arg Phe His Asp Val Leu Glu Val Lys Arg Lys Tyr
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Tyr Lys Val Asn Cys Leu Gln Phe Glu Gly Ser Val Glu Val Tyr Ala
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                                     330
Pro Phe Cys Ser Ala Lys Gln Leu Asp Trp Lys Asp Gln Gln Leu Asn
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Asn Leu Glu Lys Thr Ser Pro Ala Arg Gly Ser Cys Asn Ser Asp Thr
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Asn Thr Arg Arg Arg Ser Phe Ser Ala Val Ala Val Val Ser Ser Cys
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